hampered research efforts, resulting in remarkably limited therapeutic evidence. The EuroMyositis Registry was created to pool resources and expertise across the international IIM research community.

Objectives: To describe the phenotypic characteristics of different IIM subtypes. Associations with malignancy, interstitial lung disease (ILD), cardiac involvement and dysphagia were assessed.

Methods: Pooled data from the EuroMyositis Registry (from Belgium, China, Czech Republic, Hungary, Italy, Mexico, Norway, Sweden, Switzerland, UK, Vietnam) were obtained. Associations were assessed using logistic regression and multinomial logistic regression with polymyositis (PM) as the reference group.

Results: Data regarding 3,196 patients were analysed. The UK was the largest contributor (n=1,307). The most common diagnoses were dermatomyositis (34%), PM (32%) and connective tissue disease (CTD)-overlap myositis (15%). In those with anti-synthetase syndrome (7%), 85% had muscle weakness, 86% ILD and 58% arthritis. Overall, 43% had a myositis specific antibody, most commonly anti-Jo1 autoantibodies (20%). Glucocorticoid usage was noted in 98%. Most commonly used disease modifying agents were methotrexate (71%) and azathioprine (50%).

Malignancy occurred in 9% and was associated with a diagnosis of dermatomyositis (Relative Risk Ratio [RRR] 1.68, 95% CI 1.09–2.56, $p=0.018$). Cardiac involvement occurred in 9%, most commonly in those with CTD-overlap myositis (13%), and was associated with a higher Health Assessment Questionnaire disability index (1 versus 0.75, OR 1.40, 95% CI 1.03–1.91, $p=0.031$). Dysphagia occurred in 39% and was associated with a diagnosis of CTD-overlap myositis (RRR 2.25, 95% CI 1.61–3.15, $p<0.001$).

Conclusions: This large international cohort demonstrates the heterogeneity of IIM and the burden of associated malignancy, ILD, cardiac and gastrointestinal involvement. The EuroMyositis Registry facilitates international collaborative research outputs, underlining the benefits of harmonised data collection methodology between centres.

Acknowledgements: This work was supported by researchers at the National Institute for Health Research (NIHR) Biomedical Research Unit. The views expressed are those of the authors and not necessarily those of the UK National Health Service, the NIHR or the UK Department of Health

Disclosure of Interest: J. Lilleker: None declared, J. Vencovsky: None declared, G. Wang: None declared, L. Wedderburn Grant/research support from: The UK JDM Cohort and Biomarker study is supported by grants from the NIHR and Myositis UK, L. Diederichsen: None declared, J. Schmidt: None declared, P. Jordan: None declared, O. Benveniste: None declared, M. G. Danieli: None declared, K. Dankó: None declared, N. T. P. Thuy: None declared, M. Vazquez-Del Mercado: None declared, Ø. Molberg: None declared, B. De Paepe: None declared, J. De Bleecker: None declared, B. Maurer Grant/research support from: AbbVie, Protogen, EMD, Novartis, Roche, Actelion, N. Pipitone Speakers bureau: GRAPPA Workshop, Alfa-Wassermann, N. McHugh: None declared, Z. Betteridge: None declared, P. New: None declared, R. Cooper: None declared, W. Ollier: None declared, J. Lamb Grant/research support from: MedImmune, N. S. Krogh: None declared, I. Lundberg Grant/research support from: Astra-Zeneca, Bristol-Myers Squibb, Consultant for: Bristol-Myers Squibb, Idera, H. Chinoy Grant/research support from: MedImmune, Novartis

DOI: 10.1136/annrheumdis-2017-eular.2742

SAT0375 METABOLOMICS OF SERA REVEALS POTENTIAL BIOMARKERS OF SKIN FIBROSIS IN SYSTEMIC SCLEROSIS THAT CORRELATE WITH PRO-FIBROTIC GENE EXPRESSION IN SKIN BIOPSIES

S. Ahmed¹, M.K. Rai¹, D. Dubey², A. Rawat², D.P. Misra¹, D. Kumar², V. Agarwal¹. ¹Clinical Immunology, Sanjay Gandhi Post Graduate Institute of Medical Sciences; ²Centre for BioMedical Research, Lucknow, India

Background: There is an unmet need for biomarkers in Systemic Sclerosis (SSc). Despite its shortcomings, the modified Rodnan skin score (mRSS) has remained the standard disease assessment tool for SSc. Expression of certain genes, cartilage oligomeric matrix protein (COMP), thrombospondin-1 (THS1), interferon-induced 44 (IFI44) and sialoadhesin (SIG1), and, more recently, Tenascin-C (TNSC), have been shown to correlate with skin fibrosis. However, assessment of the expression of these genes requires a skin biopsy. Hence, we used an open-ended approach to identify a serum-based biomarker of SSc.

Objectives: To identify small molecules in serum that correlate with mRSS and profibrotic genes that are upregulated in skin of SSc patients

Methods: We obtained serum and skin biopsies from 25 consenting adult patients with SSc and serum from 25 age- and sex-similar controls. mRNA levels of five genes: COMP, THS1, IFI44, SIG1, and TNSC were estimated as fold-change relative to Glyceraldehyde 3-phosphate dehydrogenase (GAPDH), a housekeeping gene. H¹NMR (Nuclear Magnetic Resonance) based metabolomics studies were performed on the sera using standard protocols. Principal component analysis (PCoA) and Partial Least Squares Discriminant Analysis (PLSDA) were used to delineate metabolites that were different between patients and healthy controls. Then spearman correlations (ρ) of these metabolites with mRSS and the fold-expression of the five pro-fibrotic genes were estimated.

Results: H¹NMR based metabolomics identified 126 peaks that were different between patients and controls. Out of these, the levels of glycine had the best correlation with pro-fibrotic gene expression ($\rho=0.5$, $p<0.05$ for IFI44; $\rho=0.44$,

Figure 1: H¹-NMR Metabolomics data (A) PCoA plot showing metabolomics can clearly distinguish between patients of systemic sclerosis and healthy controls (B) Plot showing 20 representative metabolites that were significantly different between patients and controls; SSc: Systemic Sclerosis, HC: Healthy Controls, PUFA: Poly Unsaturated Fatty Acids; VLDL: Very Low Density Lipoproteins, GPC: Glycerophosphocholine, VIP: Variable Importance in Projection Score

$p<0.05$ for TNSC). Choline inversely correlated with SIG1 ($\rho=-0.41$; $p=0.05$) while Glycerophosphocholine correlated with mRSS ($\rho=0.50$, $p<0.05$).

Conclusions: H¹NMR based metabolomics identified glycine, choline and their metabolites as potential biomarkers for skin fibrosis in SSc. These findings require validation in a larger cohort.

References:

- [1] Farina G, Lafyatis D, Lemaire R, Lafyatis R. A four-gene biomarker predicts skin disease in patients with diffuse cutaneous systemic sclerosis. *Arthritis Rheum*. 2010 Feb;62(2):580–8.
- [2] Bhattacharyya S, Wang W, Morales-Nebreda L, Feng G, Wu M, Zhou X, Lafyatis R, Lee J, Hinchcliff M, Feghali-Bostwick C, Lakota K, Budinger GR, Raparia K, Tamaki Z, Varga J. Tenascin-C drives persistence of organ fibrosis. *Nat Commun*. 2016 Jun 3;7:11703.

Disclosure of Interest: None declared

DOI: 10.1136/annrheumdis-2017-eular.3715

SAT0376 ANTI-NT5C1A AUTOANTIBODIES ARE FREQUENT IN JUVENILE MYOSITIS AND ASSOCIATED WITH INCREASED ILLNESS SEVERITY

R. Yeker¹, I. Pinal-Fernandez¹, T. Kishi², I.N. Targoff³, F.W. Miller², L.G. Rider², A. Mammen¹. ¹Muscle Disease Unit, National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS)/National Institutes of Health (NIH); ²Environmental Autoimmunity Group, National Institute of Environmental Health Sciences (NIEHS)/National Institutes of Health (NIH), Bethesda; ³University of Oklahoma Health Sciences Center, Oklahoma City, United States

Background: Autoantibodies (Abs) against 5'-Nucleotidase, Cytosolic 1A (NT5C1A) have been portrayed as a potential diagnostic aide in distinguishing inclusion body myositis (IBM) and polymyositis (PM) in adults. However, 4–21% of dermatomyositis (DM) patients also have Abs to NT5C1A.

Objectives: The prevalence and clinical features of anti-NT5C1A Abs in juvenile-onset myositis (IIM) patients is unknown, so we sought to examine this in a large cohort.

Methods: We screened 384 juvenile IIM patients meeting probable or definite Bohan and Peter criteria for anti-NT5C1A Abs by immunoblotting for the full length NT5C1A protein in transfected and non-transfected lysates. Clinical characteristics and HLA typing were compared between juvenile IIM patients who were anti-NT5C1A positive (Ab+) and those who were anti-NT5C1A negative (Ab-).

Results: In this cohort, 29% (103) of juvenile DM, 15% (3) of juvenile PM, and 37% (15) of juvenile overlap myositis patients tested positive for anti-NT5C1A Abs. Compared with anti-NT5C1A Ab- patients, anti-NT5C1A Ab+ juvenile IIM patients showed a similar distribution of race, gender, and association with myositis-specific Abs. However, NT5C1A Ab was associated with anti-p155/140 Abs ($p=0.05$). The only observed clinical difference was an increased frequency of V- or shawl-sign rashes ever present (44% vs. 26%, $p=0.002$). Disease severity was increased in anti-NT5C1A Ab+ patients, based on more frequent hospitalizations ($p=0.02$), more medications used ($p<0.001$), and more treatment trials per year ($p<0.001$). Additionally, pulse steroids ($p<0.001$) and intravenous immunoglobulin therapy ($p=0.008$) were prescribed more frequently in anti-NT5C1A Ab+ than Ab- patients. The HLA alleles DRB1*07 (20% vs. 9%, $p<0.05$) and DQA1*0201 (21% vs. 7%, $p<0.01$) were present more frequently in anti-NT5C1A Ab- compared to Ab+ patients.

Conclusions: Anti-NT5C1A Abs are commonly present in juvenile DM and juvenile overlap myositis patients, and are present more frequently in patients with anti-p155/140 Abs, but are also seen in association with other myositis specific Abs. Consistent with data in adult IIM patients, anti-NT5C1A Abs have few distinguishing clinical features in juvenile myositis, but are associated with increased illness severity marked by increased hospitalizations and receipt of additional therapy.

Disclosure of Interest: R. Yeker: None declared, I. Pinal-Fernandez Grant/research support from: The Myositis Association, T. Kishi Grant/research support